

SEQUENCE LISTING

(1) GENERAL INFORMATION.

- (i) APPLICANT: Needleman, Philip  
Glenn, Kevin
- (ii) TITLE OF INVENTION: An Immunological Process and Constructs  
for Increasing the HDL Cholesterol Concentration by DNA  
Vaccination
- (iii) NUMBER OF SEQUENCES: 52
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Welsh & Katz, Ltd.
  - (B) STREET: 120 South Riverside Plaza, 22nd Floor
  - (C) CITY: Chicago
  - (D) STATE: IL
  - (E) COUNTRY: USA
  - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Gansch, Ph.D., Edward P.
  - (B) REGISTRATION NUMBER: 29,381
  - (C) REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (312) 655-1500
  - (B) TELEFAX: (312) 655-1501

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1446 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (viii) POSITION IN GENOME:
  - (C) UNITS: bp
- (x) PUBLICATION INFORMATION:
  - (A) AUTHORS: Drayna, Dennis  
Jannagin, Alisha Stephens  
McBean, John  
Henzel, William  
Kear, William  
Fielding, Christopher  
Lawn, Richard

(B) TITLE: Cloning and sequencing of human cholesteryl  
ester transfer protein cDNA  
(C) JOURNAL: Nature  
(D) VOLUME: 327  
(E) PAGES: 631-634  
(F) DATE: June 18-1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCTCCAAAG	3DAGCTCGCA	CGAGGCAGGC	ATCGTGTGCC	GCATCACCAA	GCCTGCCCTC	60
CTGGTGTGA	AGCAGAGAC	TGCAAGGTC	ATCCAGACCG	CCTTCCAGCG	AGCCAGCTAC	120
CCAGATATCA	CGGGCGAGAA	GGCATGATG	CTCCTTGGCC	AAGTCAAGTA	TGGGTTGCAC	180
AACATCCAGA	CGAGCCACTT	GTTCATCGCC	AGCAGCCAGG	TGGAGCTGGT	GGAAGCCAA	240
TCCATTGATG	TCTCCATCA	GAADTGTCT	GTGGTCTTCA	AGGGGACCC	GAAGTATGGC	300
TACACCACTG	CCTGGTGGCT	GGTATTGAT	CAGTCCATTG	ACTTCGAGAT	CGACTCTGCC	360
ATTACCTCC	AGATCAAC	ATAGTGACC	TGTGACTCTG	GTAGAGTGG	GACCGATGCC	420
CCCTACTGCT	AGCTGTCTT	CTATAAGCTG	CTCTGTATC	TCCAAGGGGA	GCGAGAGCT	480
GGGTGGATCA	AGCAGCTCT	CAAAATTTT	ATCTCTTCA	CCCTGAAGCT	GGTCTGAAG	540
GGACAGATCT	CAAAAGAGAT	CAATTCATC	TCTAACATCA	TGGCCGATT	TGTCCAGACA	600
AGGCTGCGCA	GCATCTTTC	AGATGAGAC	ATTGGGGTGG	ACATTTCCCT	GACAGGTGAT	660
CCCTCATCA	CAGCTCTCA	CCTGGAGTC	CATCACAAGG	GTCAATTCAT	CTACAAGAA	720
GTCTCAGAG	AGCTGCTCT	CGCCACCTT	TGCCCCACAC	TGCTGGGGGA	CTCCCGCATG	780
CTGTACTTCT	GGTCTCTCA	GGGATCTTC	CACTCGCTGG	CCAAGGTAGC	TTTCCAGGAT	840
GGCTGCTCA	TGCTGAGCT	GATGGAGAC	GAGTTCAAGG	CAGTGCTGGA	GACCTGCGGC	900
TTCAACACCA	ATCAGGAAAT	CTTCAAGAG	GTGTGGGGG	GCTTCCCCAG	CCAGGCCCAA	960
GTCACCGTCT	ACTGCTTCA	GATGCCCAAG	ATCTCCTGCC	AAAACAAGGG	AGTCGTGGTC	1020
AATCTTCAAG	TGATGGTGA	ATTCTCTTT	CCACGCCAG	ACCAGCAACA	TTCTGTAGCT	1080
TACACATTTC	AAGAGGATAT	CGTACTACC	GTCCAGGCCT	CCTATTCTAA	GAAGAGCTC	1140
TTCTTAAGCT	TCTTGGATTT	CGAGATTACA	CCAAAGACTG	TTTCCAACTT	GACTGAGAGC	1200
AGCTGGAGAT	CGATTCAGAG	CTTCTGCA	TCAATGATCA	CGCTGTGGG	CATCCCTGAG	1260
GTCATGTCTT	GGCTGGAGCT	ATTTTTTACA	GGCTCATGA	ACAGCAAAGG	CGTGAGCTTC	1320
TTTACATCA	TCAACCTTCA	GATTATCACT	CGAGATGGCT	TCTGTCTGCT	CGAGATGAC	1380
TTTGGCTCT	CTGAGAGCT	CTGGTGGAT	TTCCTCCAGA	GCTTGAGCTA	G	1431

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala Gln  
1 5 10 15  
Val Ala Val His  
2

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Ala Val Thr Phe Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val  
1 5 10 15  
Ala Tyr Arg Phe  
2

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp  
1 5 10 15  
Phe Leu Gln Ser Leu Ser  
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His Leu  
1 5 10 15  
Leu Asp Phe Gln  
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Leu Lys Gln  
1 5 10 15  
Leu Phe Thr Asn  
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu Gly Arg Val Lys Tyr  
1 5 10 15  
Gly Leu His Asn  
20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln  
1 5 10 15  
Val Thr Val His  
20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser Val  
1 5 10 15  
Ala Tyr Thr Phe  
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp  
1 5 10 15  
Phe Leu Gln Ser Leu Ser  
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu  
1 5 10 15  
Leu Asp Phe Gln  
20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Ile Lys Gln  
 1 5 10 15  
 Leu Phe Thr Asn  
 20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (E) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (I) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr  
 1 5 10 15  
 Gly Leu His Asn  
 20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (E) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (I) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
 (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAGGAAATCT TCCAGGAGCT TTCCAGAGGC CTTCCCACCG GCCAGGCCCA GGTAGCCGTC 60  
 CAC 63

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (E) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (I) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
 (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGCCGTGA CGTCCGCTT CCCCCGCCCA GATGGCCGAG AAGCTGTGGC CTACAGGTTT 60

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 66 base pairs  
  (B) TYPE: nucleic acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
  (E) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGCTGCTGC AGATGACTT CCGTTTTCCC AAGCACCTGC TGGTGGATTT CCTGCAGAGC     60  
CTGAGC     66

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 60 base pairs  
  (B) TYPE: nucleic acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
  (E) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACCACCGTCC AGGCTTCTTA CTCCAGAAA AAGCTCTTCC TACACCTCTT GGATTTCAG     60

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 60 base pairs  
  (B) TYPE: nucleic acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
  (E) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCTCTGTC ACCTCCAGGG GGAGCGCGAG CCGGGGTGGC TCAAGCAGCT CTTACAAAAC     60

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
  - (1) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACGTCAGCG GCGAGAGGGC CGTGATGCTC CTCGGCCGGG TCAAGTACGG GCTGCACAAC 60

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
  - (1) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGGAAATCT TCCAAGAGGT TGTGGCGGC TTCCCAGCC AGGCCCAAGT CACCGTCCAC 60  
TGC 63

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (viii) POSITION IN GENOME:
  - (1) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGATGGTGA AATTCTCTT TCCACGCCCA GACCAGCAAC ATTCTGTAGC TTACACATT 60



(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGCTGCTGC AGATGACTT TGGCTTCCCT GAGCACCTGC TGGTGGATT CTCCAGAGC 60  
TTGAGC 66

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACTACCGTCC AGGCTTCTA TTCTAAGAAA AAGCTCTCT TAAGCCTCTT GGATTTCAG 60

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGCTCTGCT ATCTCAAGG GGAGCGAGAG CCTGGGTGGA TCAAGCAGCT GTTCACAAAT 60

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATATCACGG GCGAGAAGGC CATGATGCTC CTTGGCCAAG TCAAGTATGG GTTGACACAAC 60

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 497 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Nagashima, M.  
McLean, J. W.  
Lawn, R. M.  
(B) TITLE: Cloning and mRNA tissue distribution of  
rabbit cholesteryl ester transfer protein  
(C) JOURNAL: J. Lipid Res.  
(D) VOLUME: 29  
(E) PAGES: 1643-1649  
(F) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala	Cys	Pro	Lys	Gly	Ala	Ser	Tyr	Glu	Ala	Gly	Ile	Val	Cys	Arg	Ile
1				5				10						15	
Thr	Lys	Pro	Ala	Leu	Leu	Val	Leu	Asn	Gln	Glu	Thr	Ala	Lys	Val	Val
			20					25					30		
Gln	Thr	Ala	Phe	Gln	Arg	Ala	Gly	Tyr	Pro	Asp	Val	Ser	Gly	Glu	Arg
			35				40					45			
Ala	Val	Met	Leu	Leu	Gly	Arg	Val	Lys	Tyr	Gly	Leu	His	Asn	Leu	Gln
			50			55					60				
Ile	Ser	His	Leu	Ser	Ile	Ala	Ser	Ser	Gln	Val	Glu	Leu	Val	Asp	Ala
65					70					75				80	
Lys	Thr	Ile	Asp	Val	Ala	Ile	Gln	Asn	Val	Ser	Val	Val	Phe	Lys	Gly
			85						90					95	
Thr	Leu	Asn	Tyr	Ser	Tyr	Thr	Ser	Ala	Trp	Gly	Leu	Gly	Ile	Asn	Gln
			100					105					110		
Ser	Val	Asp	Phe	Glu	Ile	Asp	Ser	Ala	Ile	Asp	Leu	Gln	Ile	Asn	Thr
			115				120					125			

Glu Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys  
130 135 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu  
145 150 155 160

Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu  
165 170 175

Lys Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser  
180 185 190

Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser  
195 200 205

Asp Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile  
210 215 220

Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys  
225 230 235 240

Asn Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu  
245 250 255

Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn  
260 265 270

Ser Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu  
275 280 285

Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr  
290 295 300

Asn Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln  
305 310 315 320

Ala Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln  
325 330 335

Asn Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe  
340 345 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp  
355 360 365

Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu  
370 375 380

His Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser  
385 390 395 400

Ser Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser  
405 410 415

Asn Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser  
420 425 430

Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val  
435 440 445

Ala Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile  
450 455 460

Ile Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met  
465 470 475 480

Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu  
485 490 495

Ser

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
 (C) UNITS: bp

(x) PUBLICATION INFORMATION:  
 (A) AUTHORS: Nagashima, Mariko  
 McLean, John W.  
 Lawn, Richard M.  
 (B) TITLE: Cloning and mRNA tissue distribution of  
 rabbit cholesteryl ester transfer protein  
 (C) JOURNAL: J. Lipid Res.  
 (D) VOLUME: 29  
 (E) PAGES: 1643-1649  
 (F) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCCTGTCCCA AAGGCGCTC CTACGAGGCT GGCATCGTGT GTCGCATCAC CAAGCCGCTC	60
CTCTTGGTGT TGAACCAAGA GACGGCCAAG GTGGTCCAGA CGGCCTTCCA GCGCGCTCGC	120
TATCCGGAAC TCAGCGCGCA GAGGGCCGTG ATGCTCCTCG GCCGGGTCAA GTACGGGCTG	180
CACAACCTCC AGATCAGCCA CTTGTCCATC GGCAGCAGCC AGGTGGAGCT GGTGGAGGCT	240
AAGACCATCC AGTGGGCCAT CCAGAACGTG TCCGTGGTCT TCAAGGGGAC CCTGAACTAC	300
AGCTACACCA GTGGGCTGGG GTTGGGCATC AATCAGTCTG TCGACTTCCA GATCGACTCT	360
GCCATTGACC TCAGATCAA CACAGAGCTG AACTGCGACG CTGGCAGTGT GCGCACCAAT	420
GCCCCCGAAT GTAGCTGGC TTTCCATAAA CTGCTCCTGC AACTCCAGGG GGAGCGCGAG	480
CCGGGGTGGC TCAGGAGCT CTTCAAAAC TTCATCTCTT TCACCCTGAA GCTGATTCTG	540
AAGCGAGAGG TTTCGAATGA GATCAACACC ATCTCCAACA TCATGGCTGA CTTTGTCCAG	600
ACGAGGGGCG CCAGCATCCT CTCAGATGGA GACATCGGGG TGGACATTTG CGTGACGGGG	660
GCCCTCTCCA TGAAGCCAC CTACCTGGAG TCCATCACA AGGGTCACTT CACGCACAAG	720
AACGTCTTCC AGGCTTCCC CCTCCGCGCC TTCCCGCCCG GTCTTCTGCG GGAATCCCGC	780
ATGCTCTACT TTGGTTCTC CGATCAAGTG CTCAACTCCC TGGCCAGGCG CGCTTCCAG	840
GAGGGGCTTC TGGGTTTCTC CTGACAGGG GATGAGTTCA AGAAAGTCTT GGAGACCCAG	900
GGTTTCCACA CCAAGCAGGA AATCTTCCAG GAGCTTTCCA GAGGCCTTCC CACCGGCCAG	960
GCCCAGGTAG CCGTCACTG CTTTAAGGTG CCAAGATCTT CTGCCAATA CCGGGGTGTC	1020
GTGGTGTCTT CTTGGTCTGC CGTGACGTTT CGCTTCCCCG GCCCAGATGG CCGAGAACTT	1080
GTGGCCTACA GGTGTGAGGA GGATATCATC ACCACGTCCT AGGCTCTCTA CTCCCAAGAA	1140
AAGCTCTTCC TACGCTCTTT GGATTTCAG TCGTGCCGCG CCAGCGGAAG GGCAGGCAGC	1200

```

TCAGCAAATC TCTCCGTGGC CCTCAGGACT GAGGCTAAGG CTGTTTCCAA CCTGACTGAG      1260
AGCCGCTCCG AGTCCCTGCA GAGCTCTCTC CGCTCCCTGA TCGCCACGGT GGGCATCCCG      1320
GAGGTATGCT CTCGCTCGA GGTGGCGTTC ACAGCCCTCA TGAACAGTAA AGGCCTGSAC      1380
CTCTTCGAAA TCATCAACCC CGAGATTATC ACTCTCGATG GCTGCCTGCT GCTGCAGATG      1440
GACTTCGGTT TTCDEAAGCA CCTGCTGGTG GATTTCCTGC AGAGCCTGAG CTAG              1494

```

(2) INFORMATION FOR SEQ ID NO:28:

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 amino acids  
 (E) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (I) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(X) PUBLICATION INFORMATION:

(A) AUTHORS: Drayna, Dennis  
 Jarnagin, Alisha Stephens  
 McLean, John  
 Henzel, William  
 Kohr, William  
 Fielding, Christopher  
 Lawn, Richard  
 (E) TITLE: Cloning and sequencing of human cholesteryl  
 ester transfer protein cDNA  
 (C) JOURNAL: Nature  
 (D) VOLUME: 327  
 (F) PAGES: 632-634  
 (G) DATE: June 18-1987

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys Arg Ile Thr
 1           5           10           15
Lys Pro Ala Leu Leu Val Leu Asn His Glu Thr Ala Lys Val Ile Gln
 20           25           30
Thr Ala Phe Gln Arg Ala Ser Tyr Pro Asp Ile Thr Gly Glu Lys Ala
 35           40           45
Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile
 50           55           60
Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu Ala Lys
 65           70           75           80
Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr
 85           90           95
Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Trp Leu Gly Ile Asp Gln Ser
100           105           110
Ile Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln
115           120           125
Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys Tyr
130           135           140
Leu Ser Phe His Lys Leu Leu His Leu Gln Gly Glu Arg Glu Pro
145           150           155           160

```

Gly	Trp	Ile	Lys	Gln	Leu	Phe	Thr	Asn	Phe	Ile	Ser	Phe	Thr	Leu	Lys	165	170	175
Leu	Val	Leu	Lys	Gly	Gln	Ile	Cys	Lys	Glu	Ile	Asn	Val	Ile	Ser	Asn	180	185	190
Ile	Met	Ala	Asp	Phe	Val	Gln	Thr	Arg	Ala	Ala	Ser	Ile	Leu	Ser	Asp	195	200	205
Gly	Asp	Ile	Gly	Val	Asp	Ile	Ser	Leu	Thr	Gly	Asp	Pro	Val	Ile	Thr	210	215	220
Ala	Ser	Tyr	Leu	Glu	Ser	His	His	Lys	Gly	His	Phe	Ile	Tyr	Lys	Asn	225	230	235
Val	Ser	Gln	Asp	Leu	Pro	Leu	Pro	Thr	Phe	Ser	Pro	Thr	Leu	Leu	Gly	245	250	255
Asp	Ser	Arg	Met	Leu	Tyr	Phe	Trp	Phe	Ser	Glu	Arg	Val	Phe	His	Ser	260	265	270
Leu	Ala	Lys	Val	Ala	Phe	Gln	Asp	Gly	Arg	Leu	Met	Leu	Ser	Leu	Met	275	280	285
Gly	Asp	Glu	Phe	Lys	Ala	Val	Leu	Glu	Thr	Trp	Gly	Phe	Asn	Thr	Asn	290	295	300
Gln	Glu	Ile	Phe	Gln	Glu	Val	Val	Gly	Gly	Phe	Pro	Ser	Gln	Ala	Gln	305	310	315
Val	Thr	Val	His	Cys	Leu	Lys	Met	Pro	Lys	Ile	Ser	Cys	Gln	Asn	Lys	325	330	335
Gly	Val	Val	Val	Asn	Ser	Ser	Val	Met	Val	Lys	Phe	Leu	Phe	Pro	Arg	340	345	350
Pro	Asp	Gln	Gln	His	Ser	Val	Ala	Tyr	Tyr	Phe	Glu	Glu	Asp	Ile	Val	355	360	365
Thr	Thr	Val	Gln	Ala	Ser	Tyr	Ser	Lys	Lys	Lys	Leu	Phe	Leu	Ser	Leu	370	375	380
Leu	Asp	Phe	Gln	Ile	Thr	Pro	Lys	Thr	Val	Ser	Asn	Leu	Thr	Glu	Ser	385	390	395
Ser	Ser	Gln	Ser	Ile	Gln	Ser	Phe	Leu	Gln	Ser	Met	Ile	Thr	Ala	Val	405	410	415
Gly	Ile	Ile	Glu	Val	Met	Ser	Arg	Leu	Glu	Val	Val	Phe	Thr	Ala	Leu	420	425	430
Met	Asn	Ser	Lys	Gly	Val	Ser	Leu	Phe	Asp	Ile	Ile	Asn	Pro	Glu	Ile	435	440	445
Ile	Thr	Arg	Asp	Gly	Phe	Leu	Leu	Leu	Gln	Met	Asp	Phe	Gly	Phe	Pro	450	455	460
Glu	His	Leu	Leu	Val	Asp	Phe	Leu	Gln	Ser	Leu	Ser					465	470	475

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Swenson, T. L.  
et al.,  
(P) JOURNAL: J. Biol. Chem.  
(S) VOLUME: 264  
(F) PAGES: 14318-14326  
(G) DATE: 1989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His  
1 5 10 15  
Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids  
(P) TYPE: amino acid  
(D) STRANDEDNESS: single  
(E) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

x) PUBLICATION INFORMATION:

(A) AUTHORS: Pape, Michael E.  
Rehberg, Edward F.  
Marotti, Keith R.  
Melchior, George W.  
(B) TITLE: Molecular Cloning, Sequence, and Expression  
of Cynomolgus Monkey Cholesteryl Ester Transfer  
Protein  
(P) JOURNAL: Arteriosclerosis and Thrombosis  
(S) VOLUME: 11  
(E) ISSUE: 6  
(F) PAGES: 1759-1771  
(G) DATE: Nov/Dec-1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Leu Ala Ala Thr Val Leu Thr Leu Ala Leu Leu Gly Asn Val His  
1 5 10 15  
Ala Cys Ser Lys Gly Thr Ser His Lys Ala Gly Ile Val Cys Arg Ile  
20 25 30  
Thr Lys Phe Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Ile  
35 40 45  
Gln Ser Ala Phe Gln Arg Ala Asn Tyr Pro Asn Ile Thr Gly Glu Lys  
50 55 60  
Ala Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln  
65 70 75 80  
Ile Ser His Leu Ser Ile Ala Ser Ser Arg Val Glu Leu Val Glu Ala  
85 90 95  
Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly  
100 105 110  
Thr Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Gly Leu Gly Ile Asp Gln  
115 120 125

Ser Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr  
130 135 140

Gln Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys  
145 150 155 160

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu  
165 170 175

Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu  
180 195 190

Lys Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Ile Ile Ser  
195 200 205

Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser  
210 215 220

Asp Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Ile Ile  
225 230 235 240

Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly Tyr Phe Ile Tyr Lys  
245 250 255

Asn Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Ala Leu Leu  
260 265 270

Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Gln Val Phe His  
275 280 285

Ser Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Thr Leu Ser Leu  
290 295 300

Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr  
305 310 315 320

Asn Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala  
325 330 335

Gln Val Thr Val His Cys Leu Lys Met Pro Arg Ile Ser Cys Gln Asn  
340 345 350

Lys Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro  
355 360 365

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp Ile  
370 375 380

Met Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser  
385 390 395 400

Leu Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu  
405 410 415

Ser Ser Ser Glu Ser Val Gln Ser Phe Leu Gln Ser Met Ile Thr Thr  
420 425 430

Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Ala Val Phe Thr Ala  
435 440 445

Leu Met Asn Ser Lys Gly Leu Ser Leu Phe Asp Ile Ile Asn Pro Glu  
450 455 460

Ile Ile Thr Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe  
465 470 475 480

Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
485 490



(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Pape, Michael E.  
Rehberg, Edward F.  
Marotti, Keith R.  
Melchior, George W.
- (B) TITLE: Molecular Cloning, Sequence, and Expression  
of Cynomolgus Monkey Cholesteryl Ester Transfer  
Protein
- (C) JOURNAL: Arteriosclerosis and Thrombosis
- (D) VOLUME: 11
- (E) ISSUE: 6
- (F) PAGES: 1759-1771
- (G) DATE: Nov/Dec-1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCTGGCTG CCAGGTCCT GACCTGGCC CTGCTGGGCA ATGTCCACG CTGCTC AAA	60
GGTACCTCAC ACAAGCAGG CATTGTGTC CGCATCACCA AGCTGCCCT CTGCTGTTG	120
AACCAACAGA CTGCAAGGT GATCCAGCT GCTTCCAGC GAGCCAACTA CCCAAATATC	180
ACAGGCGAGA AGGCATGAT GCTCCTTGGC CAAGTCAAGT ATGGGTTGCA CAACATCCAA	240
ATCAGCCACT TGTCCATCC CAGCAGCCGG GTGGAGCTGG TGAAGCCAA GTCCATTGAT	300
GTCTCCATTC AGAGGTGTC TGTGCTCTC AAGGGGACCC TGAAGTATG CTACACCACT	360
GCCTGGGGG TGGCAATGA TCAGCCCTT GACTTCGAGA TCGACTCTG CATTGAOCTC	420
CAGATCAACA CACACTGAC CTGTGACTCT GGTAGAGTGA GGACTGATG CCTGACTGC	480
TACCTGTCTT TCCCTAAGCT GCTCCTGAT CTCCAAGGG AGCGAGAGC CGGGTGGATC	540
AAGCACTGT TCACTAAGCT CATCTCTTC ACCCTGAAG TGGTCTGAA GGGACAGATC	600
TGCAAGAGA TCAAGTATC CTCCAACATC ATGGCCGATT TTGTCCAGAC AAGGGCTGCC	660
AGTATECTTT CAGATGGAGA CATCGGGTG GACATTTCCC TGACAGGTGA TCCCATCATT	720
ACAGCTCCTT ACCTGAGTC CCATCAAGG GTTATTTC TCTATAAGAA TGTCTGGAG	780
GACCTCCAC TCCCTACCT CTCGCCGCA CTGCTGGGG ACTCCCGAT GCTGTACTTC	840
TGGTTCTCCG AGCAAGTCT CCACTCCCTG GCAAGGTAG CTTTCCAAG TCCCGGCTC	900
ACGCTAGCC TGATGGAGA CGAGTTAAG GCAGTGTGG AGACTGGGG CTTCAACACC	960
AACCAAGAAA TCTCCAGGA GGTGTGGGC GCTTCCCCA GCCAGGCCA AGTCAAGCTC	1020
CACTGCTCA AGAGGCGAG GATCTCTGC CAAAACAAG GAGTGTGCT CAATTCTTCG	1080
GTGATGTTGA AATCTCTCT TCCAGGCCA BACCAGCAAC ACTCTGTAG TTACACATTT	1140
GAAGAGGATA TCATGAGAC CGTCCAGGC TCTATTCTA AAAAAAGCT CTTCTTAAGC	1200
CTCTTGATT TCCGATTAC ACCAAGACT GTTTCCACT TGAAGAGAG CAGCTCCAG	1260

TCCGTCCAGA GCTTCTTSCA GTCAATGATC ACCACTGTGG GCATCCCTGA GGTCATGTCT	1320
CGGCTTGAGG CAGTGTTTAC AGCCCTCATG AACAGCAAAG GCCTGAGCCT CTTGACATC	1380
ATCAATCCTG AGATTATCAC TCGAGATGGC TTCCTGCTGC TGCAGATGGA CTTTGGCTTC	1440
CCTGAGCACC TGCTGGTBSA TTTCCTCCAG AGCTTGAGCT AGAAGTCTTC AAGGACGTCA	1500
GGATGGGG	1508

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln	Glu	Ile	Phe	Gln	Glu	Val	Val	Gly	Gly	Phe	Pro	Ser	Gln	Ala	Gln
1				5				10					15		
Val Thr Val His															
20															

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val	Met	Val	Lys	Phe	Leu	Phe	Pro	Arg	Pro	Asp	Gln	Gln	His	Ser	Val
1			5					10					15		
Ala Tyr Thr Phe															
20															

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu	Leu	Leu	Gln	Met	Asp	Phe	Gly	Phe	Pro	Glu	His	Leu	Leu	Val	Asp
1				5				10					15		

Phe Leu Gln Ser Leu Ser

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu  
1 5 10 15

Leu Asp Phe Gln  
20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Ile Lys Gln  
1 5 10 15

Leu Phe Thr Asn  
20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asn Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr  
1 5 10 15

Gly Leu His Asn  
20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 183 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1      5      10      15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20      25      30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35      40      45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50      55      60
Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65      70      75      80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
 85      90      95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100      105      110
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115      120      125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130      135      140
Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145      150      155      160
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165      170      175
Gln Ser Arg Glu Ser Gln Cys
180

```

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 552 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

ATGGACATCG ACCCTATAA AGAATTGGA GCTACTGTGG AGTTACTCTC GTTTTTCCT      60
TCTGACTTCT TTCCTTCAGT ACGAGATCTT CTAGATACCG CCTCAGCTCT GTATCGGGAA      120

```

```

GCCTTAGAGT CTCCTGAGCA TTGTTACCT CACCATACTG CACTCAGGCA AGCAATTCTT      180
TGCTGGGGGG AACTAATGAC TCTAGCTACC TGGGTGGGTG TTAATTTGGA AGATCCAGCG      240
TCTAGAGACC TAGTAGTCA? TTATGTCAAC ACTAATATGG GCCTAAAGTT CAGGCAACTC      300
TTGTGGTTTC ACATTTCCTT? TCTCACTTTT GGAAGAGAAA CAGTTATAGA GTATTTGGTG      360
TCTTTCGGAG TGTGATTCT? CACTCCTCCA GCTTATAGAC CACCAAATGC CCCTATCCTA      420
TCAACACTTC CGGAGACTAC TGTTGTTAGA CGACGAGGCA GGTCCCCTAG AAGAAGAACT      480
CCCTCGCCTC GCAGACGAAG GTCTCAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGGAA      540
TCTCAATGTT AG                                                              552

```

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val
1           5           10           15
Val Ser Tyr Val Asn Thr Asn Met Gly
                20           25

```

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
1           5           10           15
Ile Glu Tyr Leu Val
                20

```

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro  
1 5 10 15  
Asn Ala Pro Ile Leu  
21

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATCCCATGG ACATCGACCC TTATAAAGAA TTTGG

35

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCAAGCTT TTAAGATTGA GATTCGCGAG ATTGAGATCT TCTG

44

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:  
GATCGAATTC ACTAGTTGGA AGATCCAGCG TCTAGAGACC TAG 43

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:  
GATCGAATTC CTCGAGCTAG AGTCATTAGT TCCCCCAGC A 41

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:  
GATTATCACT CGAGATGGGT TCCTGCTGCT GCAG 34

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:  
GATCGAATTC AGCGCTTAAG CTCTGGAGGA AATCCACCAG 40

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu	Asp	Gly	Cys	Leu	Leu	Leu	Gln	Met	Asp	Phe	Gly	Phe	Pro	Lys	His
1				5					10					15	
Leu	Leu	Val	Asp	Phe	Leu	Gln	Ser	Leu	Ser						
			20					25							

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGCCGCAACG TTCTACTAGC TCAGGCTCTG CAGGAAATCC ACCAGCAGGT G 51

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGCCGCCCAT GGCTGTCTCC AAAGGCGCCT CCTACGAGGC T 41